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FILE 'REGISTRY' ENTERED AT 11:33:01 ON 18 AUG 2004

=> S CELLOBIOHYDROLASE/CN
L1             1 CELLOBIOHYDROLASE/CN

FILE 'CAPLUS' ENTERED AT 11:33:17 ON 18 AUG 2004

=> S CELLOBIOHYDROLASE;S L1,L2
          1120 CELLOBIOHYDROLASE
           265 CELLOBIOHYDROLASES
L2        1191 CELLOBIOHYDROLASE
                 (CELLOBIOHYDROLASE OR CELLOBIOHYDROLASES)


          1278 L1
L3        1556 (L1 OR L2)

=> S THERMAL;S STABILITY;S L4(3A)L5
        943439 THERMAL
            66 THERMALS
L4      943468 THERMAL
                 (THERMAL OR THERMALS)


        586957 STABILITY
         22693 STABILITIES
L5      598024 STABILITY
                 (STABILITY OR STABILITIES)


L6       86565 L4(3A)L5

=> S LINKER;S CATALYTIC;S CELLULOSE BINDING;S DOMAIN
         15785 LINKER
          3721 LINKERS
L7       17918 LINKER
                 (LINKER OR LINKERS)


        369379 CATALYTIC
            26 CATALYTICS
L8      369388 CATALYTIC
                 (CATALYTIC OR CATALYTICS)


        317708 CELLULOSE
          4103 CELLULOSES
        318173 CELLULOSE
                 (CELLULOSE OR CELLULOSES)
        828829 BINDING
          1831 BINDINGS
        829343 BINDING
                 (BINDING OR BINDINGS)
L9        1070 CELLULOSE BINDING
                 (CELLULOSE(W)BINDING)


        229359 DOMAIN
        121679 DOMAINS
L10     289590 DOMAIN
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(DOMAIN OR DOMAINS)

=> S L7 AND L8 AND L9 AND L6
L11 2 L7 AND L8 AND L9 AND L6

=> D 1-2 CBIB ABS

L11 ANSWER 1 OF 2 CAPLUS COPYRIGHT 2004 ACS on STN
2003:717659 Document No. 139:242281 Sequences of a **linker** region of Trichoderma reesei cellobiohydrolase I gene and use for improving thermostability. Adney, William S.; Decker, Stephen R.; Mccarter, Suzanne; Baker, John O.; Nieves, Rafael; Himmel, Michael E.; Vinzant, Todd B. (USA). U.S. Pat. Appl. Publ. US 2003170861 A1 20030911, 17 pp. (English). CODEN: USXXCO. APPLICATION: US 2002-31496 20020114.

AB The invention provides sequences of a liker region between a **catalytic** domain and a **cellulose binding** domain of a modified cellobiohydrolase. A nucleic acid mol. having a nucleic acid sequence that encodes a **linker** region of exoglucanase, said nucleic acid sequence comprising the nucleic sequence 5'-GGCGGAAACCCGCCTGGCACCACC-3'.

L11 ANSWER 2 OF 2 CAPLUS COPYRIGHT 2004 ACS on STN
2001:430751 Document No. 135:104253 Do domain interactions of glycosyl hydrolases from Clostridium thermocellum contribute to protein thermostability?. Kataeva, Irina A.; Blum, David L.; Li, Xin-Liang; Ljungdahl, Lars G. (Center for Biological Resources Recovery and Department of Biochemistry and Molecular Biology, University of Georgia, Athens, GA, 30602-7229, USA). Protein Engineering, 14(3), 167-172 (English) 2001. CODEN: PRENE9. ISSN: 0269-2139. Publisher: Oxford University Press.

AB Cellulolytic and hemicellulolytic enzymes usually have a domain composition The mutual influence of a **cellulose-binding** domain (CBD) and a **catalytic** domain was investigated with cellobiohydrolase CelK and xylanase XynZ from C. thermocellum. CelK is composed of an N-terminal family IV CBD (CBDIVCelK), a family 9 glycosyl hydrolase domain (Gh9CelK) and a dockerin domain (DD). CelK without the DD, (CBDIV-Gh9)CelK and CBDIVCelK bound cellulose. The thermostability of (CBDIV-Gh9)CelK was significantly higher than that of CBDIVCelK and Gh9CelK. The temperature optima of (CBDIV-Gh9)CelK and Gh9CelK were 65 and 45°, resp. XynZ consists of an N-terminal feruloyl esterase domain (FAEXynZ), a **linker** (L), a family VI CBD (CBDVIXynZ), a DD, and a xylanase domain. FAEXynZ and (FAE-L-CBDVI)XynZ, used in the present study did not bind cellulose, but both were highly thermostable. Replacement of CBDVIXynZ with CBDIVCelK resulted in chimeras with feruloyl esterase activity and the ability to bind cellulose. CBDIVCelK-FAEXynZ bound cellulose with parameters similar to that of (CBDIV-Gh9)CelK. (FAE-L)XynZ-CBDIVCelK and FAEXynZ-CBDIVCelK had lower relative affinities and binding capacities than those of (CBDIV-Gh9)CelK. The 3 chimeras were much less thermostable than FAEXynZ and (FAE-L-CBDVI)XynZ. The results indicated that domains of glycosyl hydrolases are not randomly combined and that domain interactions affect the properties of these domain-structured enzymes.

=> S L7 AND L8 AND L9 AND L4
L12 3 L7 AND L8 AND L9 AND L4

=> S L12 NOT L11
L13 1 L12 NOT L11

=> D CBIB ABS

L13 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2004 ACS on STN
1999:1418 Document No. 130:193394 Structure and function analysis of Pseudomonas plant cell wall hydrolases. Hazlewood, Geoffrey P.; Gilbert, Harry J. (Laboratory of Molecular Enzymology, The Babraham Institute, Cambridge, CB2 4AT, UK). Progress in Nucleic Acid Research and Molecular Biology, 61, 211-241 (English) 1998. CODEN: PNMBAF. ISSN: 0079-6603. Publisher: Academic Press.

AB A review with 81 refs. Hydrolysis of the major structural polysaccharides of plant cell walls by the aerobic soil bacterium Pseudomonas fluorescens subsp. cellulosa is attributable to the production of multiple extracellular cellulase and hemicellulase enzymes, which are the products of distinct genes belonging to multigene families. Cloning and sequencing of individual genes, coupled with gene sectioning and functional anal. of the encoded proteins have provided a detailed picture of structure/function relationships and have established the cellulase-hemicellulase system of P. fluorescens subsp. cellulosa as a model for the plant cell wall degrading enzyme systems of aerobic cellulolytic bacteria. Cellulose- and xylan-degrading enzymes produced by the pseudomonad are typically modular in structure and contain **catalytic** and noncatalytic domains joined together by serine-rich **linker** sequences. The cellulases include a cellodextrinase; a β-glucan glucohydrolase and multiple endoglucanases, containing **catalytic** domains belonging to glycosyl hydrolase families 5, 9, and 45; and **cellulose-binding** domains of families II and X, both of which are present in each enzyme. Endo-acting xylanases, with **catalytic** domains belonging to families 10 and 11, and accessory xylan-degrading enzymes produced by P. fluorescens subsp. cellulosa contain **cellulose-binding** domains of families II, X, and XI, which act by promoting close contact between the **catalytic** domain of the enzyme and its target substrate. A domain homologous with NodB from rhizobia, present in one xylanase, functions as a deacetylase. Mannanase, arabinanase, and galactanase produced by the pseudomonad are single domain enzymes. Crystallog. studies, coupled with detailed kinetic anal. of mutant forms of the enzyme in which key residues have been altered by site-directed mutagenesis, have shown that xylanase A (family 10) has 8-fold α/β barrel architecture, an extended substrate-binding cleft containing at least six xylose-binding pockets and a calcium-binding site that protects the enzyme from **thermal** inactivation, **thermal** unfolding, and attack by proteinases. Kinetic studies of mutant and wild-type forms of a mannanase and a galactanase from P. fluorescens subsp. cellulosa have enabled the **catalytic** mechanisms and key **catalytic** residues of these enzymes to be identified. (c) 1998 Academic Press.

=> S THERMOSTABILITY
8219 THERMOSTABILITY
313 THERMOSTABILITIES
L14 8397 THERMOSTABILITY
(THERMOSTABILITY OR THERMOSTABILITIES)

=> S L7 AND L8 AND L9 AND L14
L15 3 L7 AND L8 AND L9 AND L14

=> S L15 NOT L12
L16 1 L15 NOT L12

=> D CBIB ABS

L16 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2004 ACS on STN

1998:76000 Document No. 128:151117 Improved **thermostability** in cellulase by production of the C-terminal truncated **catalytic** domain. Adney, William S.; Thomas, Steven R.; Baker, John O.; Himmel, Michael E.; Chou, Yat-Chen (Midwest Research Institute, USA). U.S. US 5712142 A 19980127, 19 pp., Cont.-in-part of U.S. 5,536,655. (English). CODEN: USXXAM. APPLICATION: US 1996-604913 19960222. PRIORITY: US 1989-412434 19890926; US 1992-826089 19920127; US 1993-125115 19930921; US 1994-276213 19940715.

AB The gene encoding Acidothermus cellulolyticus E1 endoglucanase is cloned and expressed in Pichia pastoris. A new modified E1 endoglucanase enzyme comprising the **catalytic** domain (residues 1-358) of the full-size, mature E1 enzyme demonstrates enhanced **thermostability** and is produced by 2 methods. The first method of producing the new modified E1 is proteolytic cleavage to remove the **cellulose binding** domain and **linker** peptide of the full size E1. The second method of producing the new modified E1 is genetic truncation of the gene encoding the full size E1 so that the **catalytic** domain is expressed in the expression product.

	L #	Hits	Search Text	DBs
1	L1	2	("4472504" OR "5298405" OR "61142960").pn.	USPAT; US-PG PUB
2	L2	1	6114296.pn.	USPAT; US-PG PUB
3	L3	506	cellobiohydrolase	USPAT; US-PG PUB
4	L4	50266	linker	USPAT; US-PG PUB
5	L5	5353	catalytic adj domain	USPAT; US-PG PUB
6	L6	453	cellulose adj binding adj domain	USPAT; US-PG PUB
7	L7	592489	thermal	USPAT; US-PG PUB
8	L8	31	L3 AND L4 AND L5 AND L6 AND L7	USPAT; US-PG PUB
9	L9	0	L3 SAME L4 SAME L5 SAME L6 SAME L7	USPAT; US-PG PUB
10	L10	7	L3 SAME L4 SAME L5 SAME L6	USPAT; US-PG PUB
11	L11	1	(L4 SAME L5 SAME L6 SAME L7) AND L3	USPAT; US-PG PUB